

Swope, Sheridan

From: Swope, Sheridan
Sent: Thursday, June 23, 2005 10:04 AM
To: Schulwitz, Paul
Subject: RE: 10/820,536

Paul,

Please Align SID 47 with any hits that have greater than 90% homology with SID 46.

This includes seqs that have 100% homology.

Thanks,
Sheridan

Noart

-----Original Message-----

From: Schulwitz, Paul
Sent: Thursday, June 23, 2005 8:23 AM
To: Swope, Sheridan
Subject: RE: 10/820,536

As far as I could tell there were no results that were in the range of 90 to 99+%.
There were results that were exactly 100% matches.
I did not feel that there was a reason to align those hits because they are exact matches.
I hope this answers your question.

Paul

-----Original Message-----

From: Swope, Sheridan
Sent: Wednesday, June 22, 2005 3:54 PM
To: Schulwitz, Paul
Subject: FW: 10/820,536

Paul, I received the results from this request.
I see where the NT data bases have been searched for SID 46.
But I don't see in the results where point (2) below has been done.
Please clarify the status of the search.
Thanks,
Sheridan

-----Original Message-----

From: Swope, Sheridan
Sent: Thursday, June 09, 2005 6:36 PM
To: STIC-Biotech/ChemLib
Cc: O'Bryen, Barbara
Subject: 10/820,536

For 10/820,536, pls search and interference search the following.

- (1) SID 46 against the NT data bases
- (2) Align SID 47 with any hits from (1) that have greater than 90% homology



STIC Search Report

Biotech-Chem Library

STIC Database Tracking Number: 156051

TO: Sheridan Swope
Location: REM-2B71/2C70
Art Unit: 1652
Monday, June 2005

Case Serial Number: 10/820536

From: Paul Schulwitz
Location: Biotech-Chem Library
REM-1A65
Phone: 571-272-2527

Paul.schulwitz@uspto.gov

Search Notes

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 10:59:17 ; Search time 0.001 Seconds
(without alignments)
3.362 Million cell updates/sec

Title: us-10-820-536-47

Perfect score: 41
Sequence: 1 cctagtcgactattctcc.....ttgaataatgctttatc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqe, 41 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : ar271714.gb_pat:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9.8	23.9	41	1 AR271714	ACCESSION:AR271714
2	8.4	20.5	41	1 AR271714	ACCESSION:AR271714

ALIGNMENTS

RESULT 1
LOCUS AR271714 41 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 32 from patent US 6503744.
ACCESSION AR271714
VERSION AR271714.1 GI:29703259
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 41)
AUTHORS Gilbert,M. and Makarchuk,W.W.
TITLE Campylobacter glycosyltransferases for biosynthesis of gangliosides
and ganglioside mimics
JOURNAL Patent: US 6503744-A 32 07-JAN-2003;
FEATURES
source
Location/Qualifiers
1..41
/organism="unknown"
/mol_type="genomic DNA"

Query Match 23.9%; Score 9.8; DB 1; Length 41;

Best Local Similarity 66.7%; Pred. No. 0;
Matches 14; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 18 TCCTTGAATAATGCTTAT 38
||| ||||| |||

DB 10 TCATATGAAAAAGTTATAT 30

RESULT 2

AR271714/c

LOCUS AR271714 41 bp DNA linear PAT 10-APR-2003
DEFINITION Sequence 32 from patent US 6503744.
ACCESSION AR271714

VERSION AR271714.1 GI:29703259
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.

REFERENCE 1 (bases 1 to 41)

AUTHORS Gilbert,M. and Makarchuk,W.W.

TITLE Campylobacter glycosyltransferases for biosynthesis of gangliosides
and ganglioside mimics

JOURNAL Patent: US 6503744-A 32 07-JAN-2003;
FEATURES
Location/Qualifiers

source
1..41
/organism="unknown"
/mol_type="genomic DNA"

Query Match 20.5%; Score 8.4; DB 1; Length 41;

Best Local Similarity 66.7%; Pred. No. 0;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 24 GAAATATGCTTATATC 41
||| ||||| |||
DB 33 GCAATTAATACTTTTTC 16

Search completed: June 23, 2005, 10:59:17
Job time : 0.001 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 23, 2005, 11:01:37 ; Search time 0.001 Seconds
(without alignments)
3.362 Million cell updates/sec

Title: us-10-820-536-47

Perfect score: 41
Sequence: 1 cctagcgcgactatttcc.....ttgaataatgccttatatc 41

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 1 seqs, 41 residues

Total number of hits satisfying chosen parameters: 2

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : us-10-820-536-46:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9.8	23.9	41	1	us-10-820-536-46
2	8.4	20.5	41	1	us-10-820-536-46

ALIGNMENTS

RESULT 1
us-10-820-536-46

Query Match 23.9%; Score 9.8; DB 1; Length 41;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 14; Conservative 0; Mismatches 7; Indels 0; Gaps 0;

QY 18 TCCTTGAATRAAGCTTTAT 38
DB 10 TCATATGAAAAAGTTATTAT 30

RESULT 2
us-10-820-536-46/c

Query Match 20.5%; Score 8.4; DB 1; Length 41;
Best Local Similarity 66.7%; Pred. No. 0;
Matches 12; Conservative 0; Mismatches 6; Indels 0; Gaps 0;

QY 24 GAAATATGCTTATATC 41
DB 33 GCAATATATTAACCTTTTTC 16

Search completed: June 23, 2005, 11:01:37
Job time : 0.001 secs